ATGGCCCAAGCCCTGCCCTGGCTCCTGCTGTGGATGGGCGCGGGAGT
GCTGCCTGCCCACGGCACCCAGCACGGCATCCGGCTGCCCCTGCGCA
GCGGCCTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGGAGAC
CGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTTGTGGAGA
TGGTGGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAG
ATGACCGTGGGCAGCCCCCCGCAGACGCTCAACATCCTGGTGGATACA
GGCAGCAGTAACTTTGCAGTGGGTGCTGCCCCCCACCCCTTCCTGCAT
CGCTACTACCAGAGGCAGCTGTCCAGCACATACCGGGACCTCCGGAAG
GGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAAGGGGAGCTGGG
CACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCGTGC
CAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCC
AACTGGGAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCT
GACGACTCCCTGGAGCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACG
TTCCCAACCTCTTCTCCCTGCAGCTTTGTGGTGCTGGCTTCCCCCTCAA
CCAGTCTGAAGTGCTGGCCTCTGTCGGAGGGAGCATGATCATTGGAGG
TATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATACACCCATCCGG
CGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATGGA
CAGGATCTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTG
TGGACAGTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGC
TGCAGTCAAATCCATCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGAT
GGTTTCTGGCTAGGAGAGCAGCTGGTGTGCTGGCAAGCAGGCACCACC
CCTTGGAACATTTTCCCAGTCATCTCACTCTACCTAATGGGTGAGGTTAC
CAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAATACCTGCGGCCA
GTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCCATCT
CACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTT
CTACGTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGC
GCTTGCCATGTGCACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCT
TTTGTCACCTTGGACATGGAAGACTGTGGCTACAACATTCCACAGACAG
ATGAGTCAACCCTCATGACCATAGCCTATGTCATGGCTGCCATCTGCGC
CCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCAGTGGCGCTGCCTC
CGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCTCCCTGC
TGAAG

FIG. 1A

CCATGCCGGCCCCTCACAGCCCCGCCGGGAGCCCGAGCCCGCTGCCCAGGCTGGC
CGCCGCSGTGCCGATGTAGCGGGCTCCGGATCCCAGCCTCTCCCCTGCTCCCGTGC
TCTGCGGATCTCCCCTGACCGCTCTCCACAGCCCGGACCCGGGGGCTGGCCCAGG
GCCCTGCAGGCCCTGGCGTCCTGATGCCCCCAAGCTCCCTCTCCTGAGAAGCCACC
AGCACCACCCAGACTTGGGGGCAGGCGCCAGGGACGGACGTGGGCCAGTGCGAGC
CCAGAGGGCCCGAAGGCCGGGGCCCACCATGGCCCAAGCCCTGCCCTGGCTCCTG
CTGTGGATGGGCGCGGGAGTGCTGCCTGCCCACGGCACCCAGCACGGCATCCGGC
TGCCCCTGCGCAGCGGCCTGGGGGGCGCCCCCCTGGGGCTGCGGCTGCCCCGGG
AGACCGACGAAGAGCCCGAGGAGCCCGGCCGGAGGGGCAGCTTTGTGGAGATGGT
GGACAACCTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGTGGGC
AGCCCCCCGCAGACGCTCAACATCCTGGTGGATACAGGCAGCAGTAACTTTGCAGT
GGGTGCTGCCCCCCACCCCTTCCTGCATCGCTACTACCAGAGGCAGCTGTCCAGCA
CATACCGGGACCTCCGGAAGGGTGTGTATGTGCCCTACACCCAGGGCAAGTGGGAA
GGGGAGCTGGGCACCGACCTGGTAAGCATCCCCCATGGCCCCAACGTCACTGTGCG
TGCCAACATTGCTGCCATCACTGAATCAGACAAGTTCTTCATCAACGGCTCCAACTGG
GAAGGCATCCTGGGGCTGGCCTATGCTGAGATTGCCAGGCCTGACGACTCCCTGGA
GCCTTTCTTTGACTCTCTGGTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAG
CTTTGTGGTGCTGGCTTCCCCCTCAACCAGTCTGAAGTGCTGGCCTCTGTCGGAGG
GAGCATGATCATTGGAGGTATCGACCACTCGCTGTACACAGGCAGTCTCTGGTATAC
ACCCATCCGGCGGGAGTGGTATTATGAGGTGATCATTGTGCGGGTGGAGATCAATG
GACAGGATCTGAAAATGGACTGCAAGGAGTACAACTATGACAAGAGCATTGTGGACA
GTGGCACCACCAACCTTCGTTTGCCCAAGAAAGTGTTTGAAGCTGCAGTCAAATCCA
TCAAGGCAGCCTCCTCCACGGAGAAGTTCCCTGATGGTTTCTGGCTAGGAGAGCAG
CTGGTGTGCTGGCAAGCAGGCACCACCCCTTGGAACATTTTCCCAGTCATCTCACTC
TACCTAATGGGTGAGGTTACCAACCAGTCCTTCCGCATCACCATCCTTCCGCAGCAA
TACCTGCGGCCAGTGGAAGATGTGGCCACGTCCCAAGACGACTGTTACAAGTTTGCC
ATCTCACAGTCATCCACGGGCACTGTTATGGGAGCTGTTATCATGGAGGGCTTCTAC
GTTGTCTTTGATCGGGCCCGAAAACGAATTGGCTTTGCTGTCAGCGCTTGCCATGTG
CACGATGAGTTCAGGACGGCAGCGGTGGAAGGCCCTTTTGTCACCTTGGACATGGA
AGACTGTGGCTACAACATTCCACAGACAGATGAGTCAACCCTCATGACCATAGCCTA
TGTCATGGCTGCCATCTGCGCCCTCTTCATGCTGCCACTCTGCCTCATGGTGTGTCA
GTGGCGCTGCCTCCGCTGCCTGCGCCAGCAGCATGATGACTTTGCTGATGACATCT
CCCTGCTGAAGTGAGGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACAC
CTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCCAGAG
CACCTCAGGACCCTCCCCACCCACCAAATGCCTCTGCCTTGATGGAGAAGGAAAAG
GCTGGCAAGGTGGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAAGAGAAGAAAG
AAGCACTCTGCTGGCGGGAATACTCTTGGTCACCTCAAATTTAAGTCGGGAAATTCT
GCTGCTTGAAACTTCAGCCCTGAACCTTTGTCCACCATTCCTTTAAATTCTCCAACCC
AAAGTATTCTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACGCAGGTTACCTTGG
CGTGTGTCCCTGTGGTACCCTGGCAGAGAAGAGACCAAGCTTGTTTCCCTGCTGGC
CAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTA
TAAACAAGCCTAACATTGGTGCAAAGATTGCCTCTTGAATT

FIG. 1B

MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRLP
RETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQT
LNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPY
TQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWE
GILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGAGFPLN
QSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEIN
GQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASST
EKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRIT
ILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVV
FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQ
TDESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDF
ADDISLLK

FIG. 2A

ETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQT
LNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPY
TQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWE
GILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGAGFPLN
QSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEIN
GQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASST
EKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRIT
ILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVV
FDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQ
TDESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDF
ADDISLLK

FIG. 2B

FIG. 3A

MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLGLRLPRETDEEPE
EPGRRGSFVEMVDNLRGKSGQGYYVEMT
VGSPPQTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPYT
QGKWEGELGTDLVSIPHGPNVTVRANI
AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQL
CGAGFPLNQSEVLASVGGSMIIGGI
DHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL
RLPKKVFEAAVKSIKAASSTEKFPD
GFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVA
TSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDED
YKDDDDK

FIG. 3B

ETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMT
VGSPPQTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPYT
QGKWEGELGTDLVSIPHGPNVTVRANI
AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQL
CGAGFPLNQSEVLASVGGSMIIGGI
DHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNL
RLPKKVFEAAVKSIKAASSTEKFPD
GFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVA
TSQDDCYKFAISQSSTGTVMGAVIME
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDED
YKDDDDK

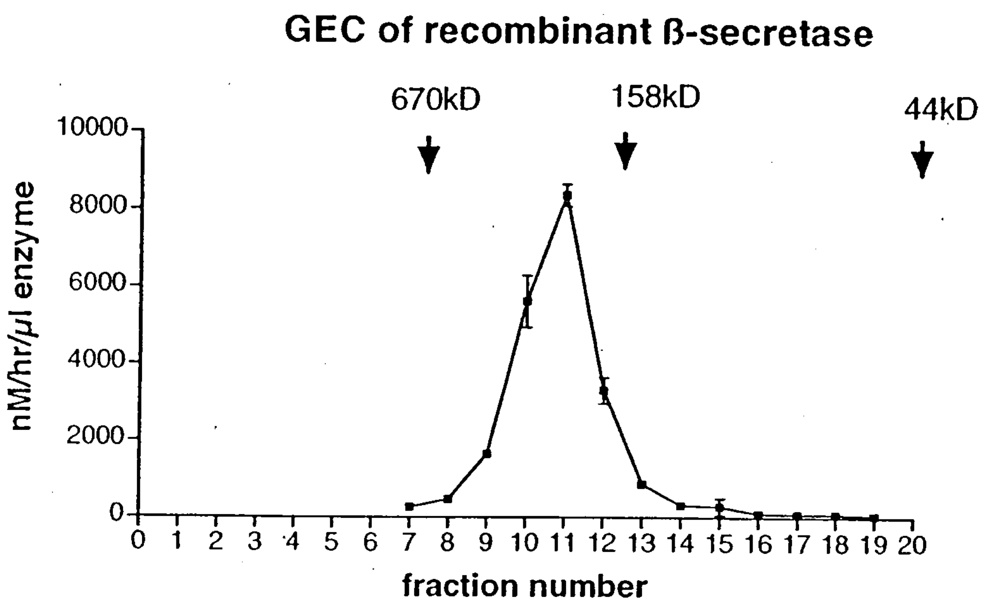
GEC of recombinant ß-secretase
670kD
158kD
44kD
nM/hr/μl enzyme
10000
8000
6000
4000
2000
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
fraction number

FIG. 4

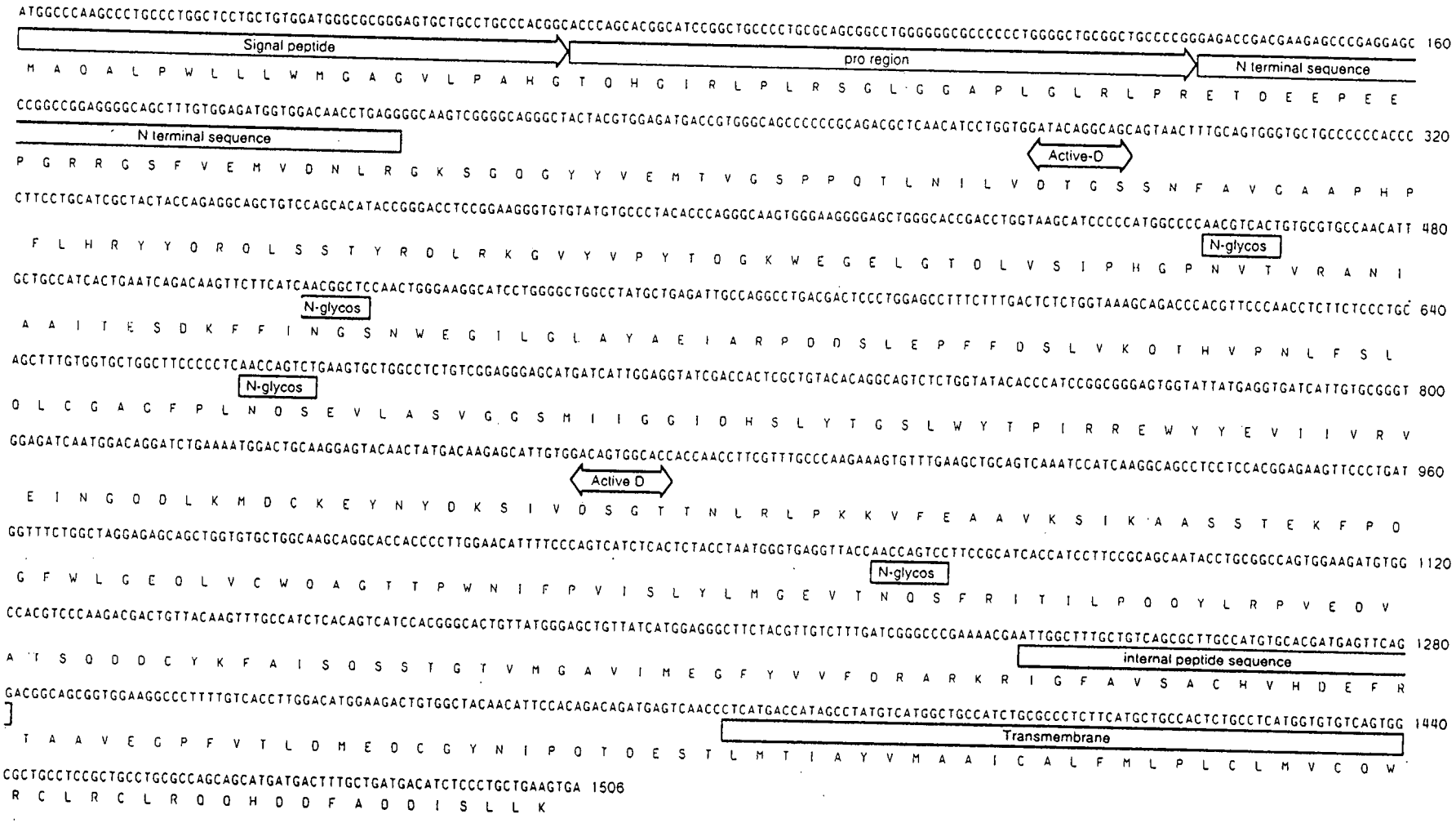
Signal peptide
pro region
N terminal sequence
N terminal sequence
Active-D
N-glycos
N-glycos
N-glycos
Active D
N-glycos
internal peptide sequence
Transmembrane

FIG. 5

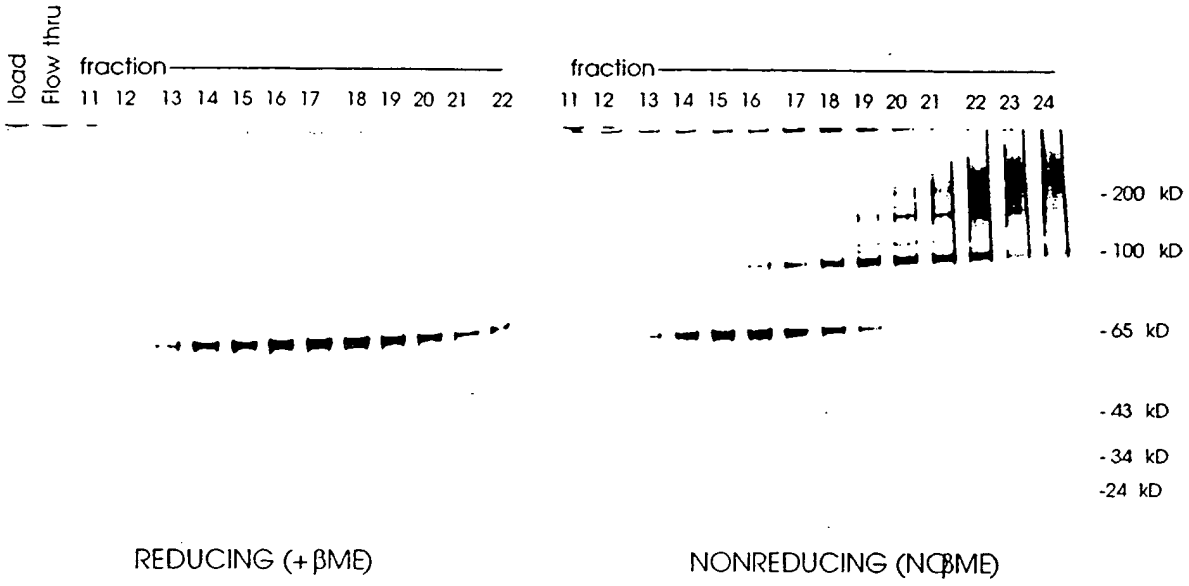

FIG. 6A

FIG. 6B

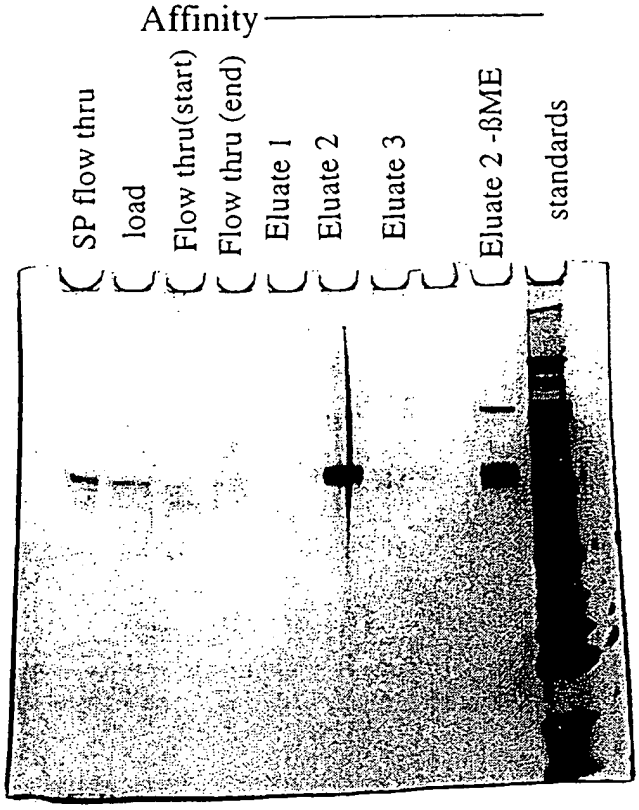
Affinity
SP flow thru
load
Flow thru(start)
Flow thru (end)
Eluate 1
Eluate 2
Eluate 3
Eluate 2 -ßME
standards

FIG. 7

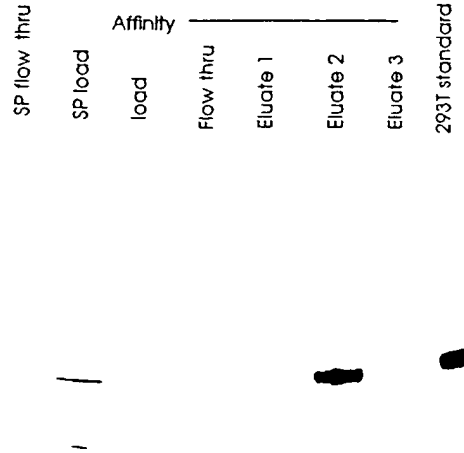
SP flow thru
SP load
load
Affinity
Flow thru
Eluate 1
Eluate 2
Eluate 3
2931 standard

FIG. 8

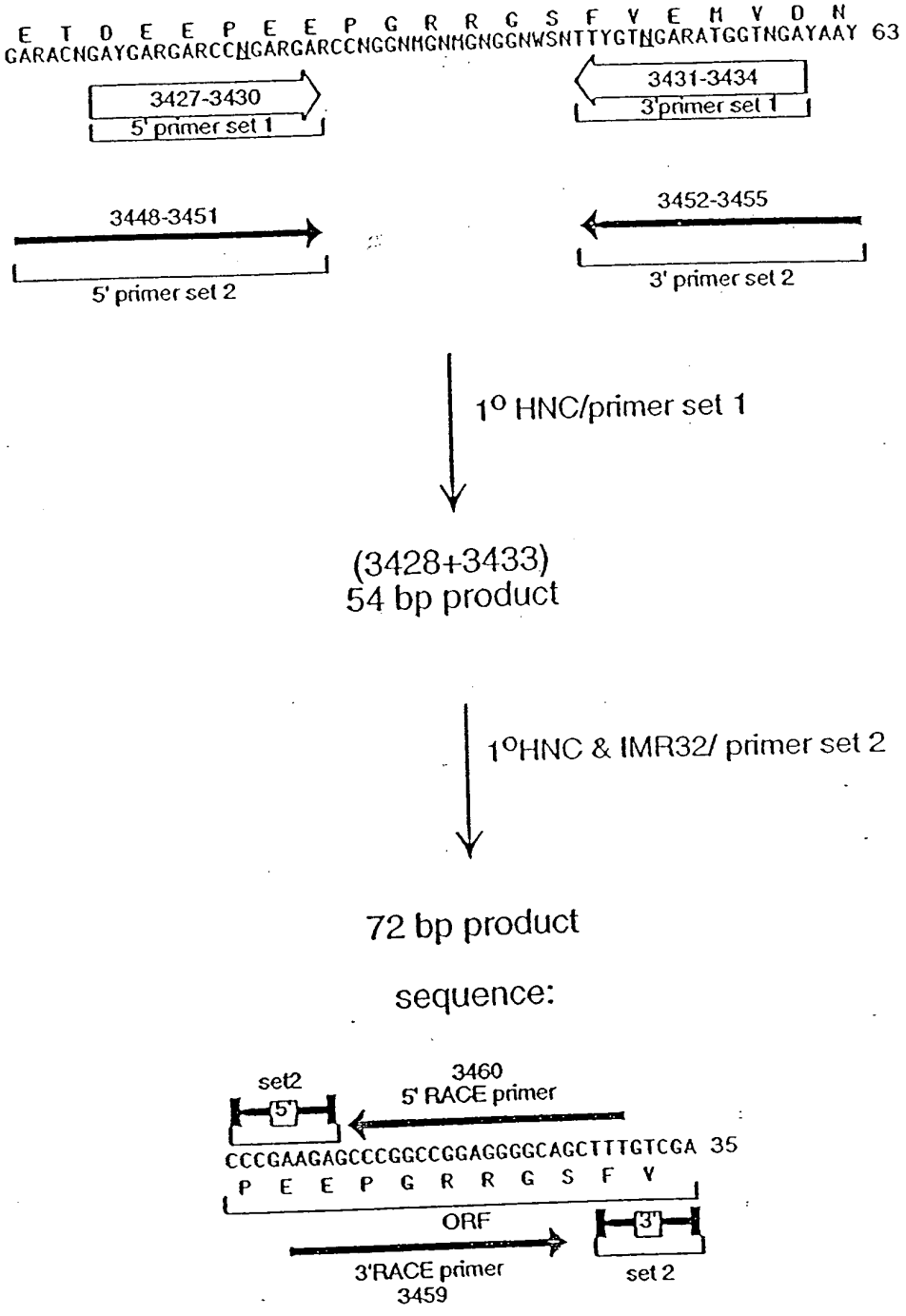
E T D E E P E E P G R R G S F V E M V D N
GARACNGAYGARGARCCNGARGARCCNGGNMGNMGNGGNWSNTTYGTNGARATGGTNGAYAAY 63
3427-3430
5' primer set 1
3431-3434
3'primer set 1
3448-3451
5' primer set 2
3452-3455
3' primer set 2
1° HNC/primer set 1
(3428+3433)
54 bp product
1°HNC & IMR32/ primer set 2
72 bp product
sequence:
set2
5'
3460
5' RACE primer
CCCGAAGAGCCCGGCCGGAGGGGCAGCTTTGTCGA 35
P E E P G R R G S F V
ORF
3'
3'RACE primer
3459
set 2

FIG. 9

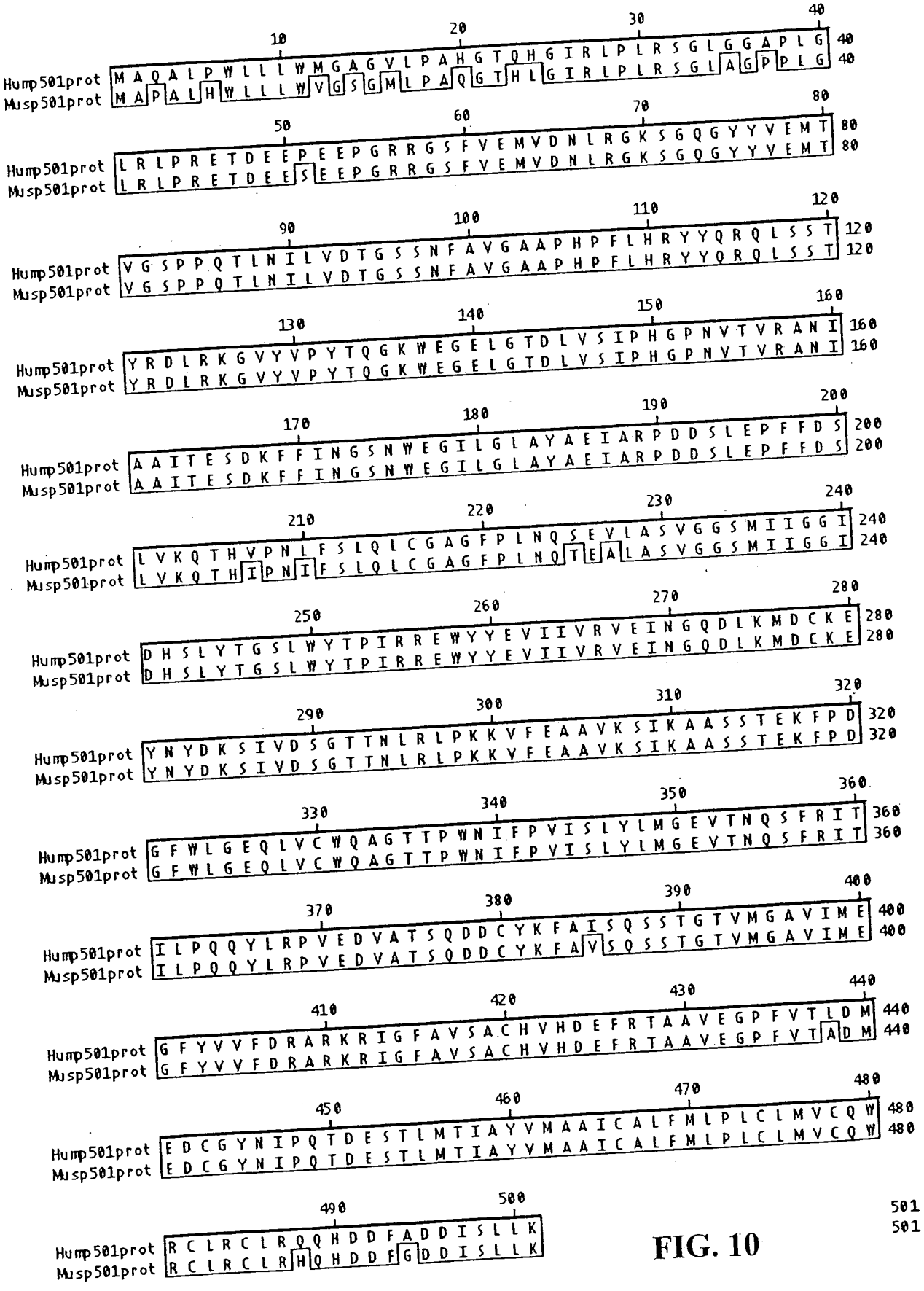
Hump501prot
Musp501prot
MAQALPWLLLWMGAGVLPAHGTQHGIRLPLRSGLGGAPLG 40
MAPALHWLLLWVGSGMLPAQGTHLGIRLPLRSGLAGPPLG 40
LRLPRETDEEPEEPGRRGSFVEMVDNLRGKSGQGYYVEMT 80
LRLPRETDEESEEPGRRGSFVEMVDNLRGKSGQGYYVEMT 80
VGSPPQTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSST 120
VGSPPQTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSST 120
YRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANI 160
YRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANI 160
AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS 200
AAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDS 200
LVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGI 240
LVKQTHIPNIFSLQLCGAGFPLNQTEALASVGGSMIIGGI 240
DHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKE 280
DHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKE 280
YNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPD 320
YNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPD 320
GFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRIT 360
GFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRIT 360
ILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIME 400
ILPQQYLRPVEDVATSQDDCYKFAVSQSSTGTVMGAVIME 400
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDM 440
GFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTADM 440
EDCGYNIPQTDESTLMTIAYVMAAICALFMLPLCLMVCQW 480
EDCGYNIPQTDESTLMTIAYVMAAICALFMLPLCLMVCQW 480
RCLRCLRQQHDDFADDISLLK 501
RCLRCLRHQHDDFGDDISLLK 501

FIG. 10

CTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTACTCT
TGGATCGGAAACCCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCT
GAGCGAGTCCGCATCGACCGGATCGGAAAACCTCTCGACTGTTGGGGTGAG
TACTCCCTCTCAAAAGCGGGCATGACTTCTGCGCTAAGATTGTCAGTTTCC
AAAAACGAGGAGGATTTGATATTCACCTGGCCCGCGGTGATGCCTTTGAGG
GTGGCCGCGTCCATCTGGTCAGAAAAGACAATCTTTTTGTTGTCAAGCTTG
AGGTGTGGCAGGCTTGAGATCTGGCCATACACTTGAGTGACAATGACATCC
ACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACTGCAGGTCG
ACTCTAGACCC

FIG. 11A

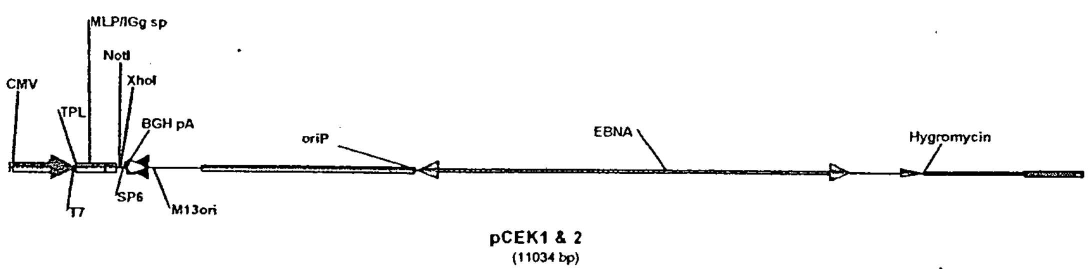

FIG. 11B

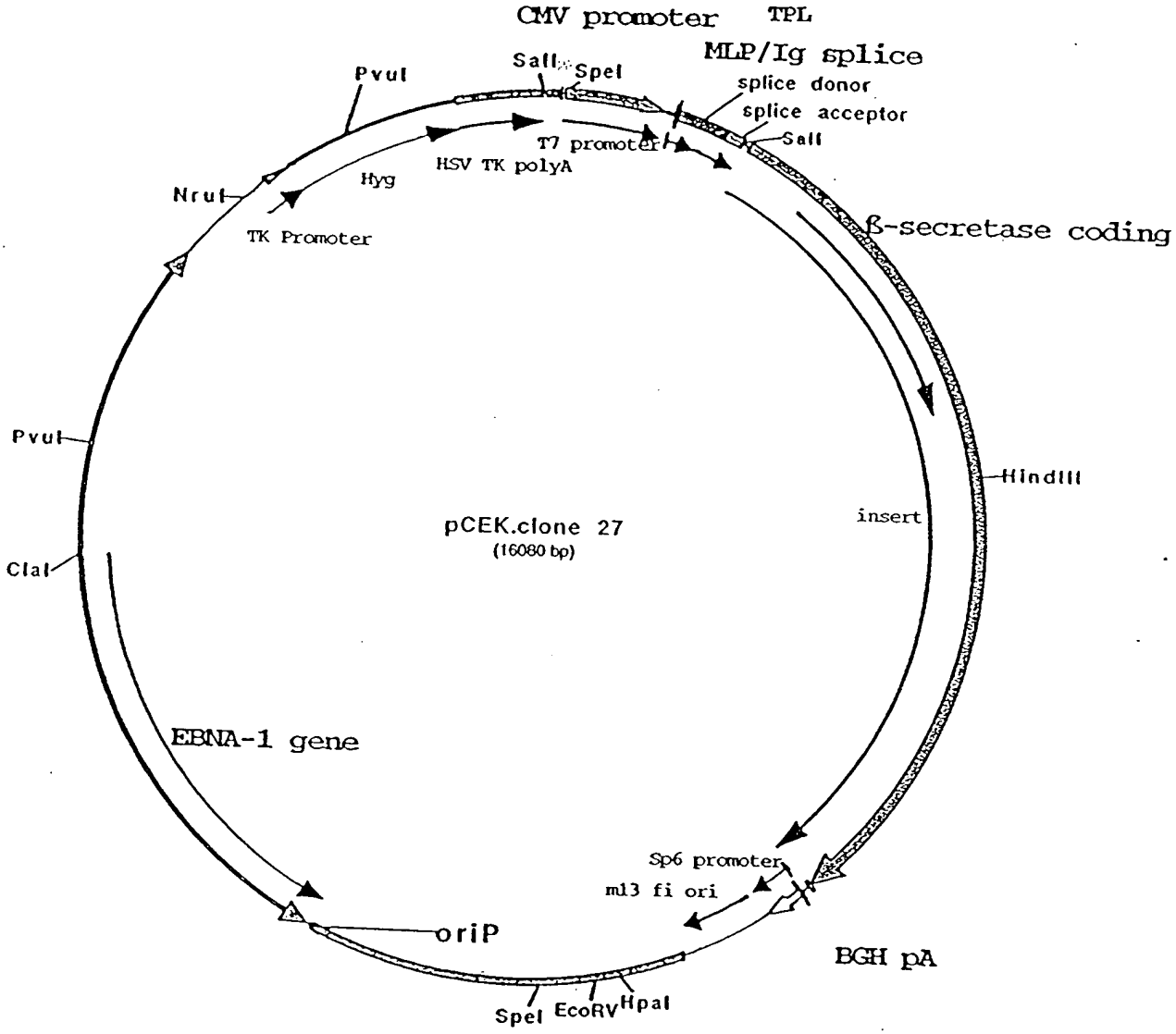
CMV promoter
TPL
MLP/Ig splice
splice donor
splice acceptor
SalI
SpeI
PvuI
T7 promoter
HSV TK polyA
Hyg
NruI
TK Promoter
ß-secretase coding
HindIII
insert
pCEK.clone 27
(16080 bp)
PvuI
ClaI
EBNA-1 gene
Sp6 promoter
ml3 fi ori
oriP
BGH pA
SpeI
EcoRV
HpaI

FIG. 12

FIG. 13A

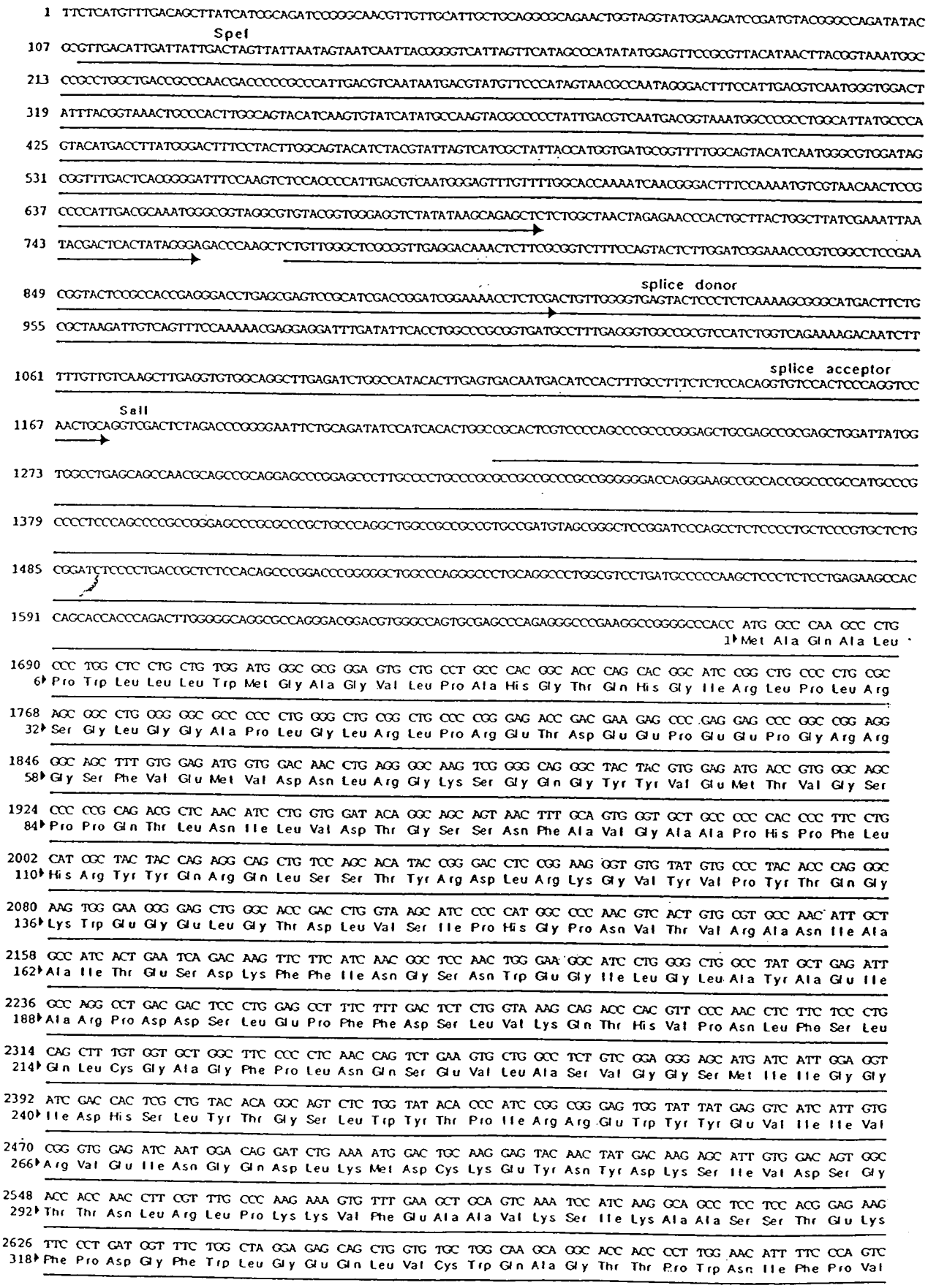

FIG. 13B

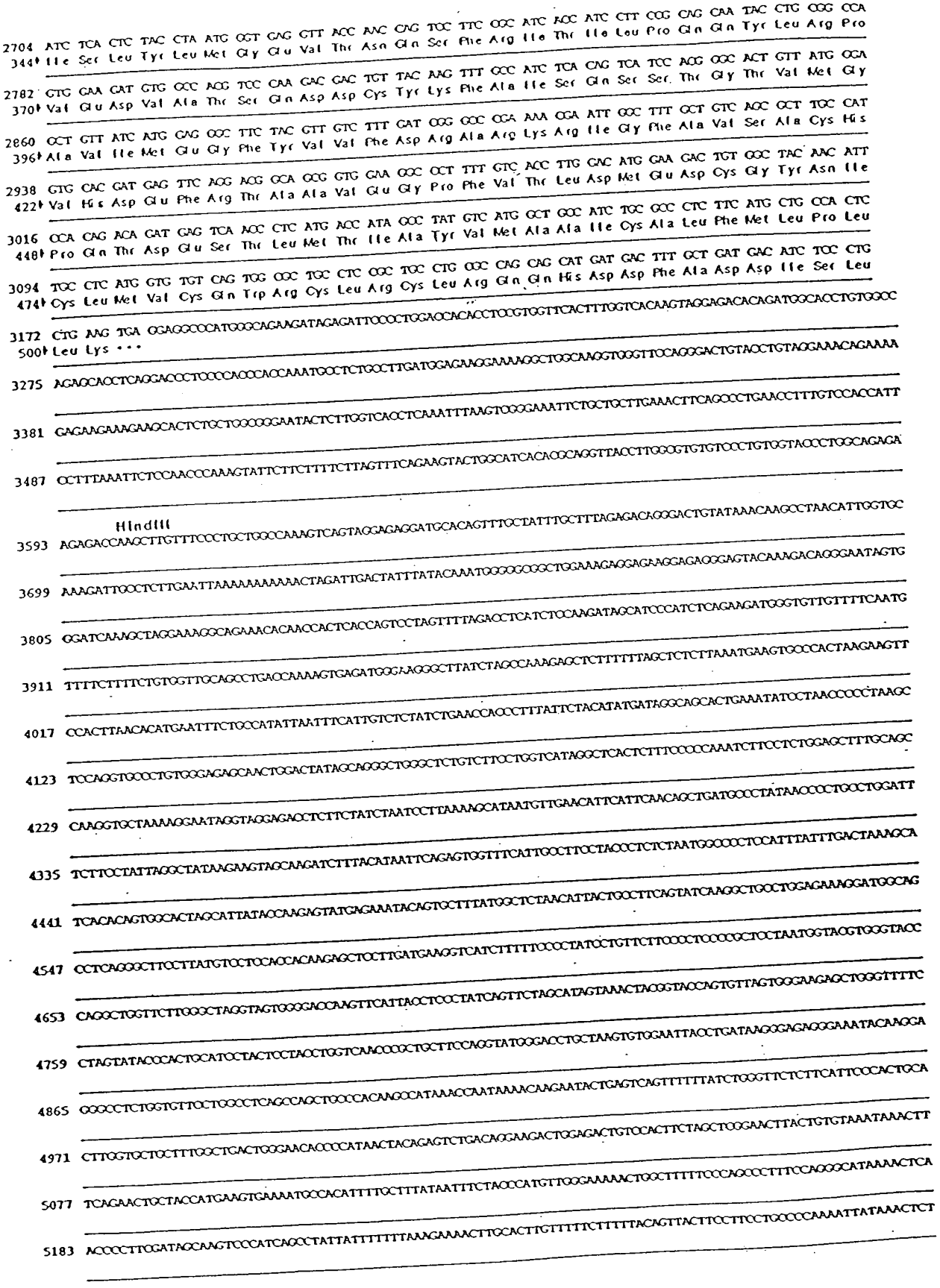
2704 ATC TCA CTC TAC CTA ATG GGT GAG GTT ACC AAC GAG TCC TTC GGC ATC AGC ATC CTT CGG GAG GAA TAC CTG CGG CCA
344 Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Glu Ser Phe Arg Ile Thr Ile Leu Pro Glu Glu Tyr Leu Arg Pro
2782 GTG GAA GAT GTG GCC AGG TCC GAA GAC GAC TGT TAC AAG TTT GCC ATC TCA GAG TCA TCC AGG GGC ACT GTT ATG GGA
370 Val Glu Asp Val Ala Thr Ser Glu Asp Asp Cys Tyr Lys Phe Ala Ile Ser Glu Ser Ser Thr Gly Thr Val Met Gly
2860 GCT GTT ATC ATG GAG GGC TTC TAC GTT GTC TTT GAT GGG GGC GGA AAA GGA ATT GGC TTT GCT GTC AGC GCT TGC CAT
396 Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His
2938 GTG CAC GAT GAG TTC AGG AGG GCA GCG GTG GAA GGC GCT TTT GTC ACC TTG GAC ATG GAA GAC TGT GGC TAC AAC ATT
422 Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile
3016 CCA CAG ACA GAT GAG TCA ACC CTC ATG ACC ATA GGC TAT GTC ATG GCT GGC ATC TGC GGC CTC TTC ATG CTG CCA CTC
448 Pro Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro Leu
3094 TGC CTC ATG GTG TGT CAG TGG CGC TGC CTC CGC TGC CTG GGC CAG CAG CAT GAT GAC TTT GCT GAT GAC ATC TCC CTG
474 Cys Leu Met Val Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser Leu
3172 CTG AAG TGA GGAGGCCCATGGGCAGAAGATAGAGATTCCCCTGGACCACACCTCCGTGGTTCACTTTGGTCACAAGTAGGAGACACAGATGGCACCTGTGGCC
500 Leu Lys ***
3275 AGAGCACCTCAGGACCCTCCCCACCCACCAAATGGCTCTGCCTTGATGGAGAAGGAAAAGGCTGGCAAGGTGGTTCCAGGGACTGTACCTGTAGGAAACAGAAAA
3381 GAGAAGAAAGAAGCACTCTGCTGGGGGGAATACTCTTGGTCACCTCAAATTTAAGTGGGGAAATTCTGCTGCTTGAAACTTCAGCCCTGAACCTTTGTCCACCATT
3487 CCTTTAAAATTCTCCAACCCAAAGTATTCTTCTTTTCTTAGTTTCAGAAGTACTGGCATCACACCCAGGTTACCTTGGGGTGTGTCCCTGTGGTACCCTGGCAGAGA
HindIII
3593 AGAGACCAAGCTTGTTTCCCTGCTGGCCAAAGTCAGTAGGAGAGGATGCACAGTTTGCTATTTGCTTTAGAGACAGGGACTGTATAAACAAGCCTAACATTGGTGC
3699 AAAGATTGCCTCTTGAATTAAAAAAAAAAAACTAGATTGACTATTTATACAAATGGGGGGGGCTGGAAAGAGGAGAAGGAGAGGAGTACAAAGACAGGGAATAGTG
3805 GGATCAAAGCTAGGAAAGGCAGAAACACAACCACTCACCAGTCCTAGTTTTAGACCTCATCTCCAAGATAGCATCCCATCTCAGAAGATGGGTGTTGTTTTCAATG
3911 TTTTCTTTTCTGTGGTTGCAGCCTGACCAAAAGTGAGATGGGAAGGGCTTATCTAGCCAAAGAGCTCTTTTTTAGCTCTCTTAAATGAAGTGCCCACTAAGAAGTT
4017 CCACTTAACACATGAATTTCTGCCATATTAATTTCATTGTCTCTATCTGAACCACCCTTTATTCTACATATGATAGGCAGCACTGAAATATCCTAACCCCCTAAGC
4123 TCCAGGTGCCCTGTGGGAGAGCAACTGGACTATAGCAGGGCTGGGCTCTGTCTTCCTGGTCATAGGCTCACTCTTTCCCCCAAATCTTCCTCTGGAGCTTTGCAGC
4229 CAAGGTGCTAAAAGGAATAGGTAGGAGACCTCTTCTATCTAATCCTTAAAAGCATAATGTTGAACATTCATTCAACAGCTGATGCCCTATAACCCCTGCCTGGATT
4335 TCTTCCTATTAGGCTATAAGAAGTAGCAAGATCTTTACATAATTCAGAGTGGTTTCATTGCCTTCCTACCCTCTCTAATGGCCCCTCCATTTATTTGACTAAAGCA
4441 TCACACAGTGGCACTAGCATTATACCAAGAGTATGAGAAATACAGTGCTTTATGGCTCTAACATTACTGCCTTCAGTATCAAGGCTGCCTGGAGAAAGGATGGCAG
4547 CCTCAGGGCTTCCTTATGTCCTCCACCACAAGAGCTCCTTGATGAAGGTCATCTTTTTCCCCTATCCTGTTCTTCCCCTCCCCGCTCCTAATGGTACGTGGGTACC
4653 CAGCCTGGTTCTTGGGCTAGGTAGTGGGGACCAAGTTCATTACCTCCCTATCAGTTCTAGCATAGTAAACTACGGTACCAGTGTTAGTGGGAAGAGCTGGGTTTTC
4759 CTAGTATACCCACTCCATCCTACTCCTACCTGGTCAACCCCCTGCTTCCAGGTATGGACCTGCTAAGTGTGGAATTACCTGATAAGGGAGAGGGAAATACAAGGA
4865 GGGCCTCTGGTGTTCCTGGCCTCAGCCAGCTGCCCACAAGCCATAAACCAATAAAACAAGAATACTGAGTCAGTTTTTTATCTGGGTTCTCTTCATTCCCACTGCA
4971 CTTGGTGCTCCTTTGGCTGACTGGGAACACCCCATAACTACAGAGTCTGACAGGAAGACTGGAGACTGTCCACTTCTAGCTGGGAACTTACTGTGTAAATAAACTT
5077 TCAGAACTCCTACCATGAAGTGAAAATGCCACATTTTGCTTTATAATTTCTACCCATGTTGGGAAAAACTGGCTTTTTCCCAGCCCTTTCCAGGGCATAAAACTCA
5183 ACCCCTTCGATAGCAAGTCCCATCAGCCTATTATTTTTTTAAAGAAAACTTGCACTTGTTTTTCTTTTTACAGTTACTTCCTTCCTGCCCCAAAATTATAAACTCT

FIG. 13C

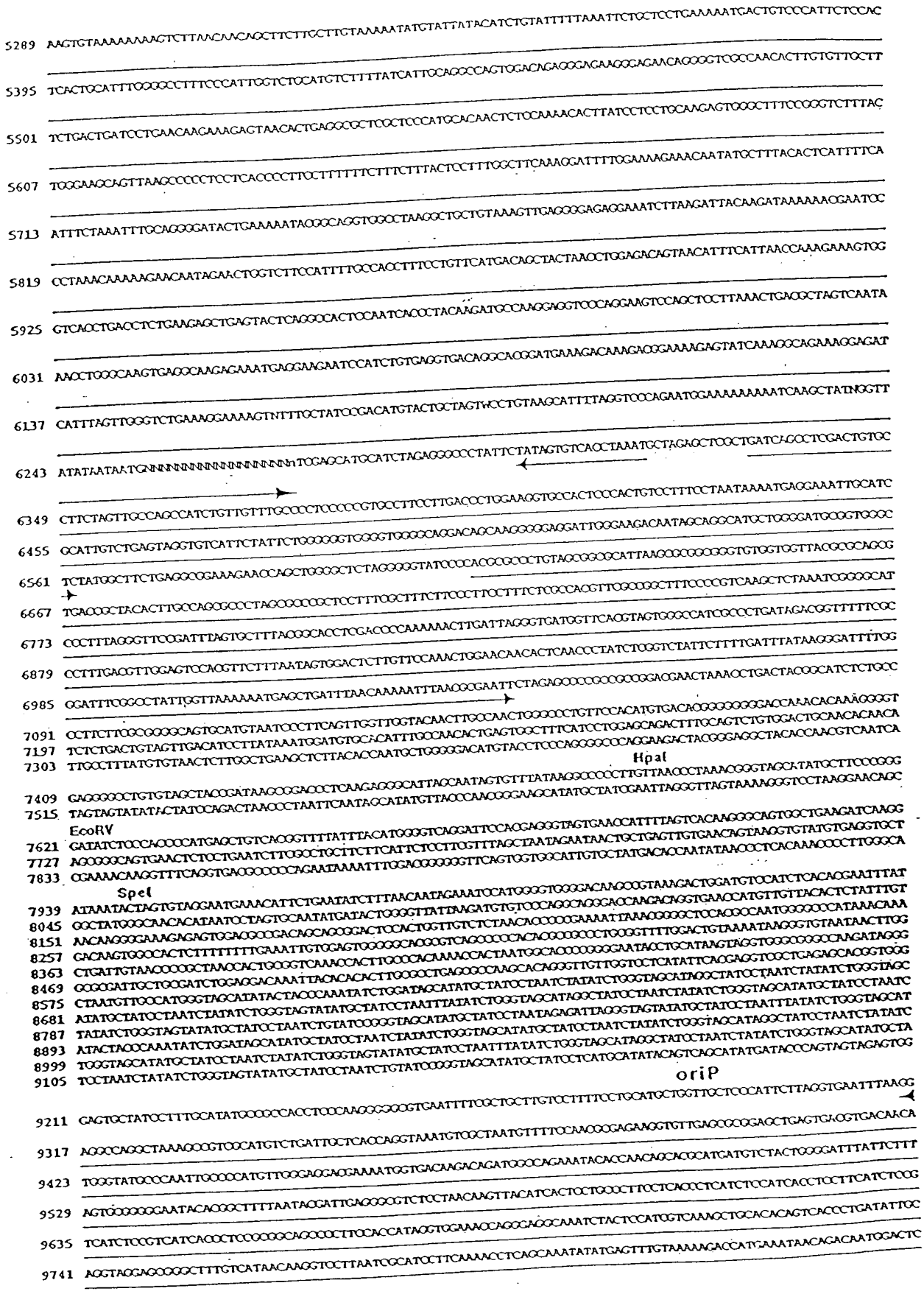
5289
5395
5501
5607
5713
5819
5925
6031
6137
6243
6349
6455
6561
6667
6773
6879
6985
7091
7197
7303
HpaI
7409
7515
EcoRV
7621
7727
7833
SpeI
7939
8045
8151
8257
8363
8469
8575
8681
8787
8893
8999
9105
oriP
9211
9317
9423
9529
9635
9741

FIG. 13D

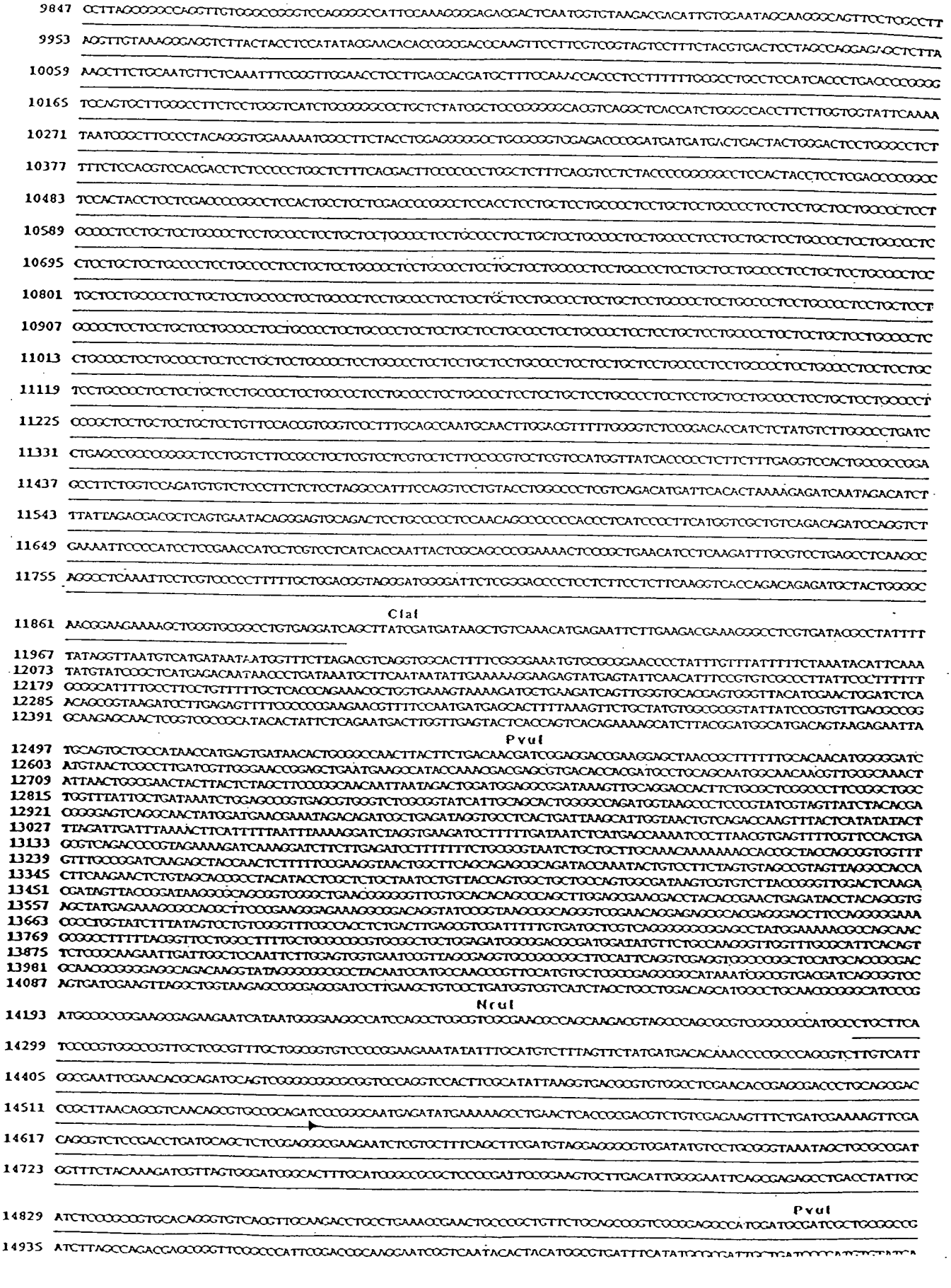

FIG. 13E

```
15041  CTGGCAAACTGTGATGGACGACACCGTCAGTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTGCAC
15147  GCGGATTTCGGCTCCAACAATGTCCTGACGGACAATGGCCGCATAACAGCGGTCATTGACTGGAGCGAGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACA
15253  TCTTCTTCTGGAGGCCGTGGTTGGCGGGTATGGAGCAGCAGACGCGCTACTTCGAGCGGAGGCATCCGGAGCTTGCAGGATCGCCGCGGCTCCGGGCGTATATGCT
15359  CCGCATTGGTCTTGACCAACTCTATCAGAGCTTGGTTGACGGCAATTTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCAATCGTCCGATCCGGAGCCGGG
15465  ACTGTCGGGCGTACACAAATCGCCCGCAGAAGCGCGGCCGTCTGGACCGATGGCTGTGTAGAAGTACTCGCCGATAGTGGAAACGGGAGATGGGGGAGGCTAACTG
15571  AAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTTC
15677  GGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGG
15783  CCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCACTGGCCCCGTGGGTTAGGGACGGGGTCCCCCATGGGGAATGGTTTATGGTTCGTGGGGG
15889  TTATTATTTTGGGCGTTGCGTGGGGTCTGGTCCACGACTGGACTGAGCAGACAGACCCATGGTTTTTGGATGGCCTGGGCATGGACCGCATGTACTGGCGCGACAC
                                                                                                    SalI
15995  GAACACCGGGCGTCTGTGGCTGCCAAACACCCCCGACCCCCAAAAACCACCGCGCGGATTTCTGGCGTGCCAAGCTAGTCGACCAA
```

CTGTTGGGCTCGCGGTTGAGGACAAACTCTTCGCGGTCTTTCCAGTACTCTTGGATCGGAAAC
CCGTCGGCCTCCGAACGGTACTCCGCCACCGAGGGACCTGAGCGAGTCCGCATCGACCGGAT
CGGAAAACCTCTCGACTGTTGGGGTGAGTACTCCCTCTCAAAAGCGGGCATGACTTCTGCGCT
AAGATTGTCAGTTTCCAAAAACGAGGAGGATTTGATATTCACCTGGCCCGCGGTGATGCCTTT
GAGGGTGGCCGCGTCCATCTGGTCAGAAAAGACAATCTTTTTGTTGTCAAGCTTGAGGTGTGG
CAGGCTTGAGATCTGGCCATACACTTGAGTGACAATGACATCCACTTTGCCTTTCTCTCCACAG
GTGTCCACTCCCAGGTCCAACTGCAGGTCGACTCTAGACCC

FIG. 14A

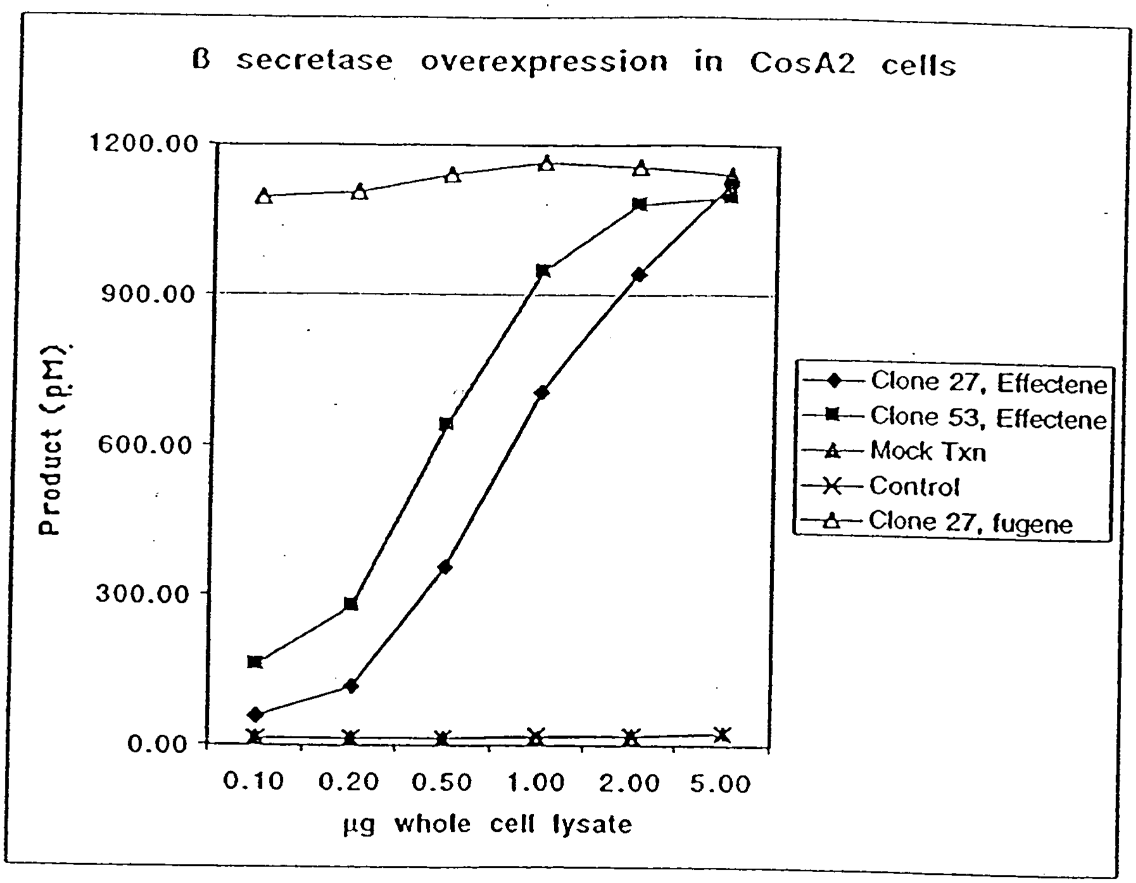

FIG. 14B

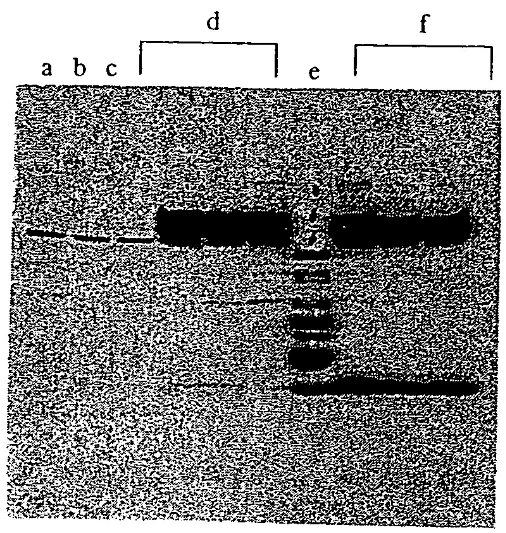

FIG. 15A

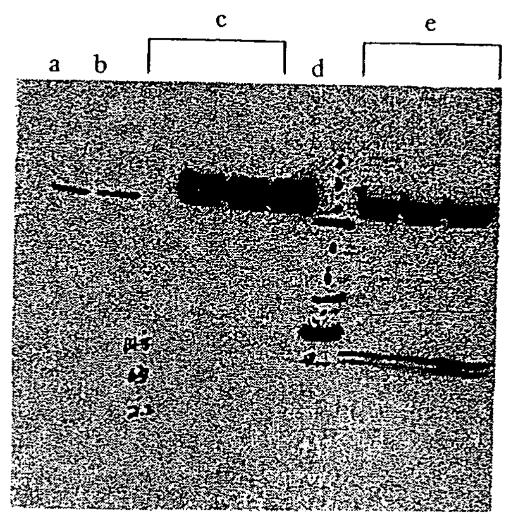

FIG. 15B

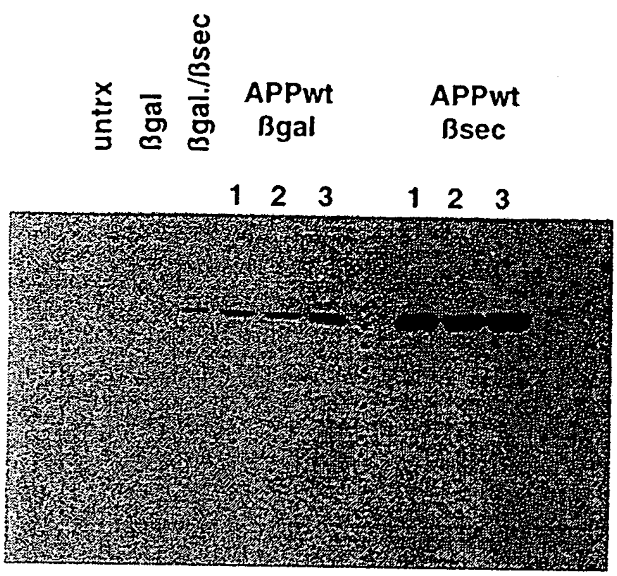

FIG. 16A

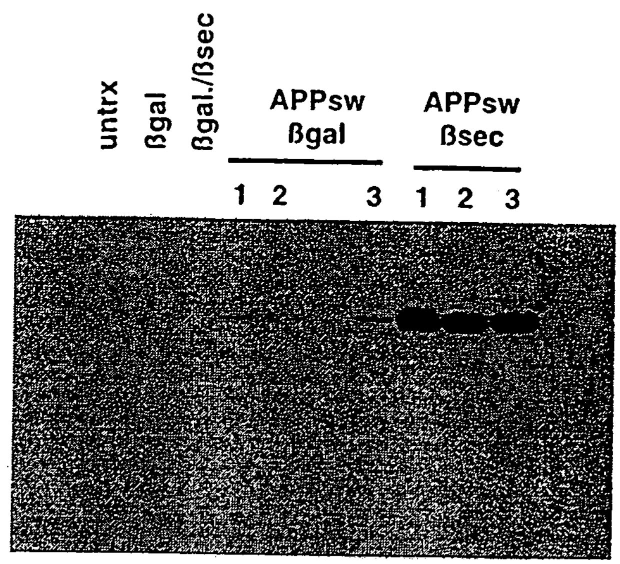

FIG. 16B

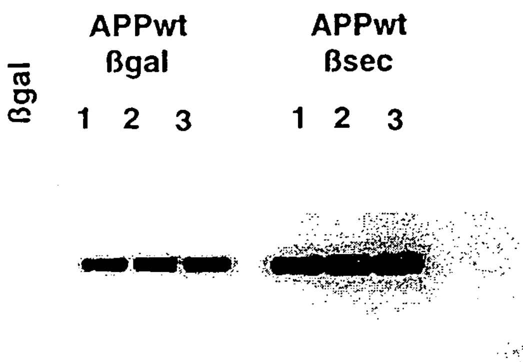

FIG. 17A

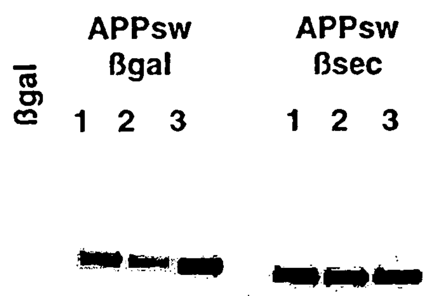

FIG. 17B

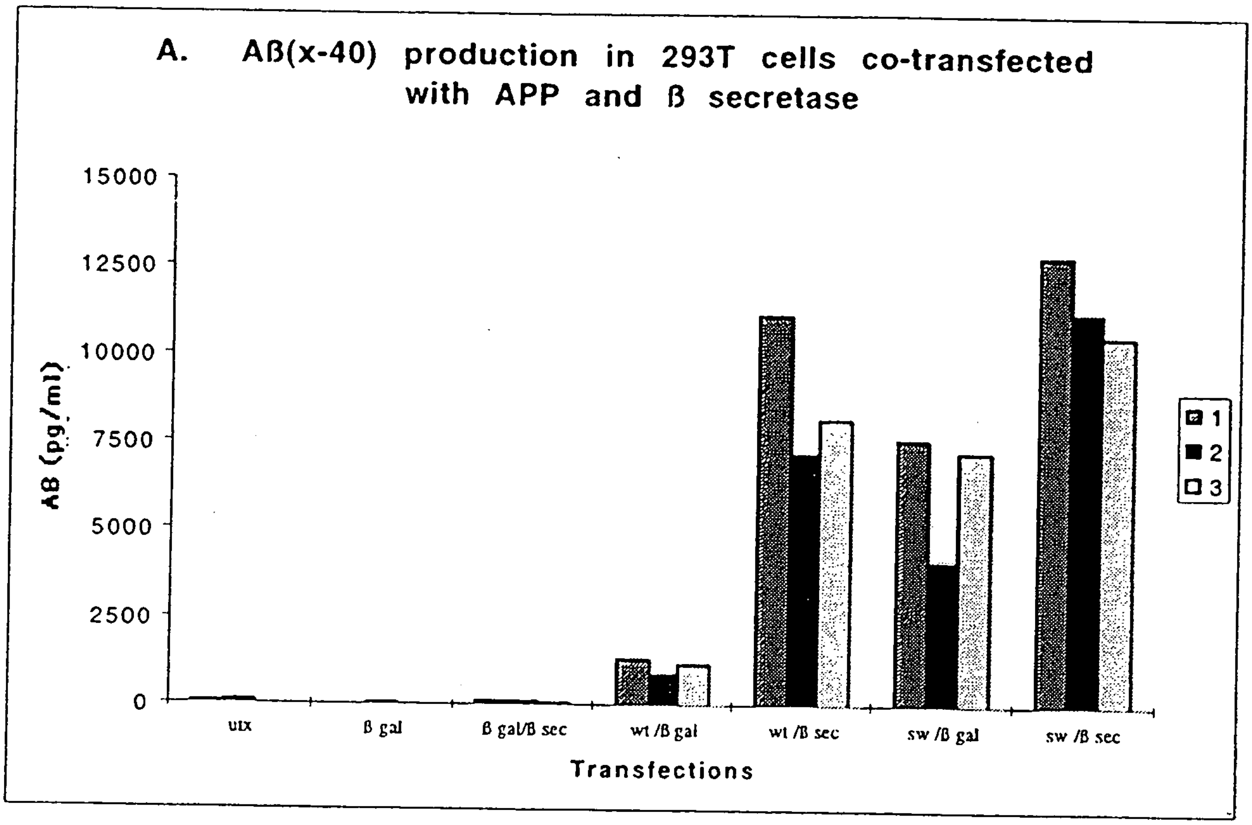
A. Aß(x-40) production in 293T cells co-transfected with APP and ß secretase
15000
12500
10000
7500
5000
2500
0
Aß (pg/ml)
1
2
3
utx
ß gal
ß gal/ß sec
wt /ß gal
wt /ß sec
sw /ß gal
sw /ß sec
Transfections

FIG. 18

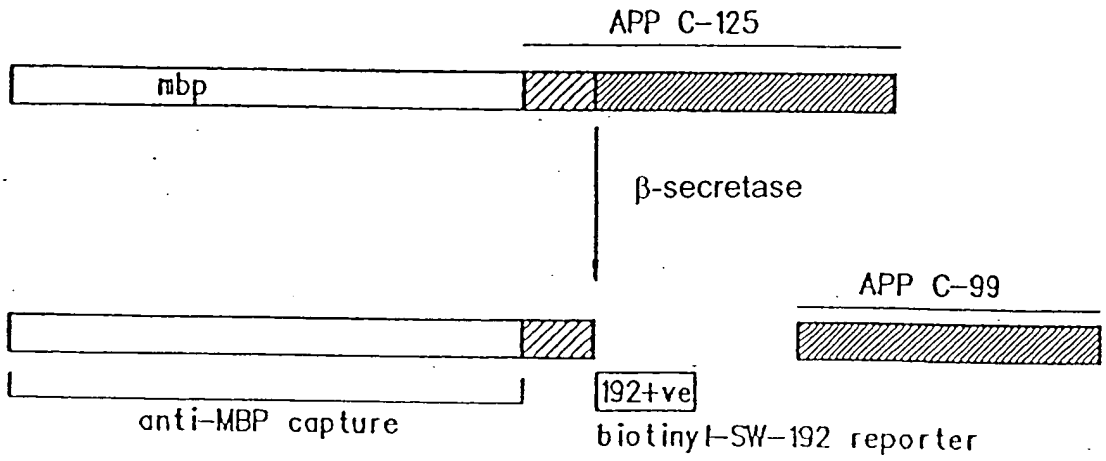

FIG. 19A

Wild-Type Sequence	....Val-Lys-Met-Asp...
Swedish Sequence	....Val-Asn-Leu-Asp...

FIG. 19B

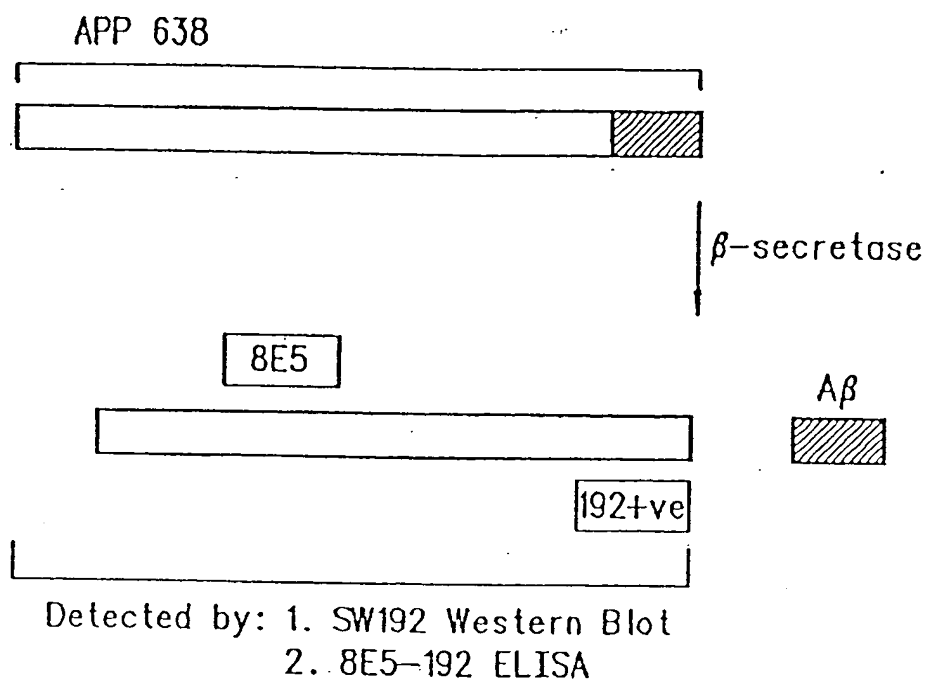

FIG. 20

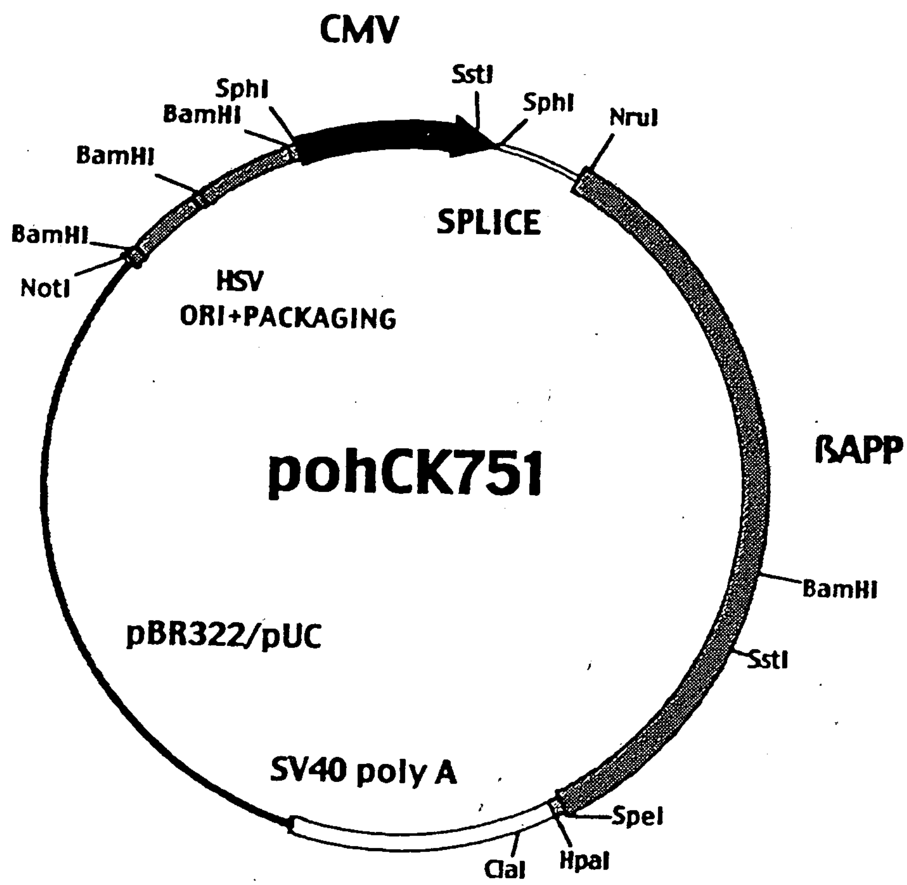

FIG. 21